IN THE SPECIFICATION

Please delete the current "Sequence Listing" and insert, after the Abstract, the enclosed "Sequence Listing," pages 1-30.

On page 1, lines 2-3, please delete the current priority information as follows:

~~This filing is a regular U.S. Patent Application resulting from the conversion of provisional applications.~~

and insert the following:

This application is a divisional application of U.S.S.N. 08/887,977, filed July 3, 1997, now allowed, which claims benefit of U.S.S.N. 60/021,664, filed July 5, 1996; U.S.S.N. 60/028,329, filed October 11, 1996; and U.S.S.N. 60/048,593, filed June 4, 1997. All the above-mentioned applications are incorporated herein by reference.

At the top of pages 1 and 135, please delete the present title as follows:

~~MAMMALIAN CHEMOKINE REAGENTS~~

and insert the following title:

ANTIBODIES THAT BIND CHEMOKINE TECK

On page 90, lines 7-25, please substitute the present text with the following text:

O. Measurement of TECK mRNA expression by RT-PCR

RNA's from sorted thymic dendritic cells or fetal thymuses were prepared with the RNeasy total RNA kit (Quiagen, Chatsworth, CA), following the manufacturer's instructions. First strand cDNAs were generated by reverse transcription with a random hexamer in a 10 μl reaction and 1 μl of this reaction was used as a template for PCR. TECK expression was compared to the expression of hypoxanthine-guanine phosphoribosyl transferase (HPRT) . Primer sequences were as follows: TECK: 5' primer, 5'CCTTCAGGTATCTGGAGAGGAGATC3' (SEQ ID NO: 20; nucleotides 58-72 of SEQ ID NO: 1) and 3' primer, 5'CACGCTTGTACTGTTGGGGTTC3' (SEQ ID NO: 21; complement of nucleotides 447-468 of SEQ ID NO: 1), HPRT: 5' primer, 5'GTAATGATCAGTCAACGGGGGAC3' (SEQ ID NO: 17) and 3' primer, 5'CCAGCAAGCTTGCAACCTTAACCA3' (SEQ ID NO: 18). Samples were submitted to 25 cycles of amplification, each composed of 94 C for 1 min., 57 C for 30 s and 72 C for 2 min. PCR products were then separated by electrophoresis in 2% agarose gels and stained with ethidium bromide.

On page 98, line 34 to page 99, line 9, please amend as follows:

C. DNA sequencing and bioinformatics

The nucleotide sequence of CRAM was determined using an ABI 377 automated sequencer and standard techniques. DNA sequence analyses were performed using Sequencher 3.0 (Gene Codes

Corporation, Ann Arbor, MI) and MacVector 6.0 (Oxford Molecular Group). Comparisons to GenBank databases were performed using the BLAST program on web-based servers: ~~(http://www.ncbi.nlm.nih.gov/BLAST/ and http://www.genome.ad.jp/SIT/BLAST.html)~~. Sequence alignments and phylogenetic analyses utilized ClustalW 1.6 (Higgins, et al. (1996) Methods in Enzymology 266:383) and TreeViewPPC 1.2 (Page (1996) Computer Applications in the Biosciences 12:357).

On page 99, lines 10-32, please substitute the present text with the following text:

D. Analysis of CRAM mRNA expression
Multiple-tissue Northern blots were purchased from Clontech (Palo Alto, CA). Poly(A)+ RNA from human monocytes was used for RNA blot analysis. cDNA libraries from human cells (5 μg) in the pSPORT vector (Life Technologies) were digested with SalI and NotI to release cDNA inserts, electrophoresed on 1% agarose gels, and subjected to Southern blot transfer/hybridization. Hybridizations with ^{32}P-labeled CRAM DNA fragments encoding the C-terminal 144 amino acids of the predicted ORF were done at 65° C in ExpressHyb (Clontech, Palo Alto, CA) for 2 hr, followed by two stringent washes at 50° C in 0.1X SSC, 0.1% SDS for 45 min. Hybridization was detected using a STORM 860 phosphorimager (Molecular Dynamics, Sunnyvale, CA). Reverse transcriptase PCR (RT-PCR) was performed with Superscript II reverse transcriptase (Life Technologies) and Taq DNA polymerase (Boehringer-Mannheim, Indianapolis, IN). PCR was for 35 cycles of 95° C/45 sec, 62° C/30 sec, 72° C/60 sec. Primers specific for exon 1 (5'-AGACGCTTCAGAGATCCTCTGGAGGCC; SEQ ID NO: 22) or exon 2 (5'-GAAGCTGCTTCGGGGGGTGAGCAAAC; SEQ ID NO: 23) were used in conjunction with an exon 3-specific primer (5'-CAAACACAGCAGAGCAGAGTGATGGCACC; SEQ ID NO: 24) for amplification.

On page 99, line 33 to page 100, line 9, please amend as follows:

E. Chromosomal localization
PCR was performed on genomic DNA from the 83 cell lines of the Stanford Human Genome Center G3 radiation hybrid panel (Research Genetics, Huntsville, AL) using CRAM primers: (5'-GTGTCCTGGCATGGGTAACAGCC; SEQ ID NO: 25) and (5'-CGGTGGAATGGTCAGGTTCTTCCC; SEQ ID NO: 26) as previously described for the GeneBridge 4 radiation hybrid panel (Samson, et al. (1996) Genomics 36:522). Data correlating the presence or absence of PCR product to each cell line were entered into the RHserver (Stanford Human Genome Center;

~~http://shgc.stanford.edu/RH/~~). Co-localized STSs were identified on the human physical map using the Entrez server (National Center for Biotechnology Information~~;~~ ~~http://www3.ncbi.nlm.nih.gov/Entrez/~~).

On page 135, please delete the second paragraph (lines 14-20) as follows:

~~This filing is a regular U.S. Patent Application resulting from the conversion of provisional applications DX0589P, USSN 60/021,664, filed July 5, 1996; DX0589P1, USSN 60/028,329, filed October 11, 1996; DX0589P2 (Wang, et al.) no Application Number yet assigned, filed June 4, 1997; each of which is incorporated herein by reference, and priority claimed to.~~